

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:45:24 ; Search time 11.0727 Seconds

(without alignments)
977.656 Million cell updates/sec

Title: US-09-988-971-2

Perfect score: 1351

Sequence: 1 MGSLSRRKSLPSPLSSSV.....RESLSFYISLNDKAVSLDDA 261

Scoring table: BLOSUM62

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 374.5 | 27.7 | 511 | 1 LYN_HUMAN | P07948 homo sapien |
| 2 | 371.5 | 27.5 | 511 | 1 LYN_HUMAN | P25911 mus musculus |
| 3 | 371.5 | 27.5 | 511 | 1 LYN_RAT | Q07014 rattus norv |
| 4 | 364.5 | 27.0 | 526 | 1 HCK_HUMAN | P08631 homo sapien |
| 5 | 362 | 26.8 | 504 | 1 HCK_MACACA | Q95M30 macaca fasc |
| 6 | 357.5 | 26.5 | 503 | 1 HCK_RAT | P50545 rattus norv |
| 7 | 356.5 | 26.4 | 504 | 1 BLK_HUMAN | P51451 homo sapien |
| 8 | 356 | 26.4 | 524 | 1 HCK_MOUSE | P08103 mus musculus |
| 9 | 345.5 | 25.6 | 498 | 1 BLK_MOUSE | P16277 mus musculus |
| 10 | 344 | 25.5 | 508 | 1 LCK_HUMAN | P06240 mus sapien |
| 11 | 342.5 | 25.4 | 508 | 1 LCK_MOUSE | P06240 mus musculus |
| 12 | 337 | 24.9 | 507 | 1 LCK_CHICK | P42683 gallus gall |
| 13 | 323.5 | 23.9 | 537 | 1 YES_CHICK | P10936 xenopus lae |
| 14 | 321 | 23.8 | 541 | 1 YES_XENLA | P09324 gallus gall |
| 15 | 319.5 | 23.6 | 536 | 1 YES_HUMAN | P06241 homo sapien |
| 16 | 319.5 | 23.6 | 543 | 1 YES_HUMAN | P07947 homo sapien |
| 17 | 316.5 | 23.4 | 529 | 1 FGR_HUMAN | P09769 homo sapien |
| 18 | 315 | 23.3 | 544 | 1 YES_XIPHE | P14052 xenopus lae |
| 19 | 314.5 | 23.3 | 536 | 1 FYN_XENLA | P00567 xenopus lae |
| 20 | 313 | 23.2 | 533 | 1 YES_AVIS1 | P00567 xenopus lae |
| 21 | 312 | 23.2 | 533 | 1 FYN_MOUSE | P35688 mus musculus |
| 22 | 309.5 | 22.9 | 546 | 1 FYN_XIPHE | P27446 xiphophorus |
| 23 | 309.5 | 22.9 | 541 | 1 YES_MOUSE | Q04736 mus musculus |
| 24 | 307 | 22.7 | 517 | 1 FGR_MOUSE | P14234 mus musculus |
| 25 | 305 | 22.6 | 535 | 1 YRK_CHICK | Q02977 gallus gall |
| 26 | 304 | 22.5 | 539 | 1 YES_CANFA | Q28923 canis fami |
| 27 | 301.5 | 22.3 | 533 | 1 FYN_CHICK | Q05876 gallus gall |
| 28 | 294 | 21.8 | 506 | 1 SRK_SPOLA | P42690 spongilla 1 |
| 29 | 290.5 | 21.5 | 526 | 1 SRC_AVIS1 | P00523 avian sarco |
| 30 | 290.5 | 21.5 | 532 | 1 SRC_CHICK | P00523 gallus gall |
| 31 | 290.5 | 21.5 | 552 | 1 SRC_DOMME | P00528 drosophila |
| 32 | 290.5 | 21.5 | 557 | 1 SRC_AVIS1 | P14085 avian sarco |
| 33 | 290.5 | 21.5 | 587 | 1 SRC_AVIS2 | P15054 avian sarco |

| | | | | | |
|----|-------|------|-----|--------------|---------------------|
| 34 | 288.5 | 21.4 | 568 | 1 SRC_AVIS1 | P14084 avian sarco |
| 35 | 281.5 | 20.8 | 535 | 1 SRC_RAT | Q9M031 rattus norv |
| 36 | 280.5 | 20.8 | 526 | 1 SRC_XSVSR | P00524 rous sarcom |
| 37 | 280.5 | 20.8 | 535 | 1 SRC_HUMAN | P12931 homo sapien |
| 38 | 280 | 20.7 | 509 | 1 STR_HYDRA | P17713 hydra atten |
| 39 | 278.5 | 20.6 | 531 | 1 SRC2_XENLA | P13116 xenopus lae |
| 40 | 277.5 | 20.5 | 526 | 1 SRC_RSVR | P00528 rous sarcom |
| 41 | 275.5 | 20.4 | 540 | 1 SRC_MOUSE | P05480 mus musculus |
| 42 | 273.5 | 20.2 | 531 | 1 SRC1_XENLA | P13115 xenopus lae |
| 43 | 272.5 | 20.2 | 526 | 1 SRC_XSVH | P25020 rous sarcom |
| 44 | 271 | 20.1 | 505 | 1 SRK1_SPOLA | P42686 spongilla 1 |
| 45 | 261 | 19.3 | 545 | 1 FGR_FSVGR | P00544 feline sarc |

ALIGNMENTS

RESULT 1
ID LYN_HUMAN STANDARD; PRT; 511 AA.
AC P07948;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
CN LYN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8712710; PubMed=3561390;
RA Yamaneh Y., Fukushima S.-I., Senda K., Sukegawa J., Miyajima N.,
Matsubara K.-I., Yamamoto T., Toyoshima K.;
RT "The yes-related cellular gene lyn encodes a possible tyrosine kinase
RT similar to p56lck.";
RT Mol. Cell. Biol. 7:237-243(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94171041; PubMed=8125304;
RA Rider L.G., Raben N., Miller L., Jelsama C.;
RT "The CDNA encoding two forms of the LYN protein tyrosine kinase are
RT expressed in rat mast cells and human myeloid cells.";
RL Gene 138:219-222(1994).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; LYN A (SHOWN HERE) AND LYN B;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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CC or send an email to license@isb.ch).
CC -----
CC EMBL: M16038; AAA59540.1; -;
CC EMBL: M79321; AAB50019.1; -;
CC PIR: A26719; TWHTLY.
CC HSSP: P08631; IAD5.
CC Genew; HGN:6735; LYN.
CC MIM; 165120; -;
CC Interpro; IPR000719; Euk_pkinase.
CC Interpro; IPR000980; SH2.
CC Interpro; IPR001452; SH3.
CC Interpro; IPR001245; Tyr_pkinase.
CC Pfam; PF00017; SH2; 1.

DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00069; Kinase; 1.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_kinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SMO0252; SH2; 1.
 DR SMART: SMO0326; SH3; 1.
 DR SMART: SMO0219; TYKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00001; SH2; 1.
 DR PROSITE: PS00002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 FT INIT MET 0 BY SIMILARITY.
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 2 PALMITATE (BY SIMILARITY).
 FT DOMAIN 62 122 SH3.
 FT DOMAIN 128 225 SH2.
 FT DOMAIN 246 500 PROTEIN_KINASE.
 FT NP_BIND 252 260 ATP (BY SIMILARITY).
 FT BINDING 274 274 ATP (BY SIMILARITY).
 FT ACT_SITE 366 366 BY SIMILARITY.
 FT MOD_RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 507 507 PHOSPHORYLATION (BY SIMILARITY).
 FT VAR_SIT 42 MISSING (IN ISOPROM LYN B).
 SQ SEQUENCE 511 AA; 56442 MW; 8419CD461204B364 CnC64;

Query Match 27.7%; Score 374.5; DB 1; Length 511;
 Best local Similarity 40.3%; Pred. No. 1.8e-24;
 Matches 81; Conservative 36; Mismatches 75; Indels 9; Gaps 3;

QY 6 SRKSLPSPLSSVSGGVNMEARSKAVNALGSPGAEISRLGEPTLYSD 65
 Db 37 SNKQRPVPE-SQLPGQRQCTDPEEGDLYALVYDGIHPDLSRKKEKVKUEH 95
 QY 66 GDMWTVLSEVSGREYNI PSYVAVK-SSHGWL EYGLSRKAEILLPNNPGAFIR 121
 Db 96 GEWMAKAKSLITKSGCFI PSNYVAKLNTLETSEWFFKITKQAEQLAPNSGAFILR 155
 QY 122 ESQTRGSGYSVLRSRPAWMDIRYRHICLDNGWLYISPLRTPSLQAVDYSGLAD 181
 Db 156 ESETLKGSFSLVADDPVAVGDIKIKIRSLDNGYIISPRITPCISDMIKRYQKAD 215
 QY 182 DICCLKEPCVQLQRAGPLPK 202
 Db 216 GLCRLEKACI---SPKPK 232

RESULT 2

LYN_MOUSE

ID LYN_MOUSE STANDARD; PRT; 511 AA.
 AC P25911; Q62127;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
 GN LYN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9120688; PubMed=1710766;
 RA Stanley E., Ralph S.J., McGwen S., Boulet I., Holtzman D.A.,
 RA Lock P., Dunn A.R.;
 RT "Alternatively spliced murine lyn mRNAs encode distinct proteins";
 RL Mol. Cell. Biol. 11:3399-3406 (1991).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91203857; PubMed=2017160;
 RA Yi T., Bolen J.B., Ihle J.N.;
 RT "Hematopoietic cells express two forms of lyn kinase differing by 21
 RT amino acids in the amino terminus";
 RL Mol. Cell. Biol. 11:2391-2398 (1991).
 RN [3]
 RP SEQUENCE OF 363-431 FROM N.A.
 RX MEDLINE=90152381; PubMed=2482828;
 RA Wilks A.F., Kuban R.R., Hovens C.M., Ralph S.J.;
 RT "The application of the polymerase chain reaction to cloning members
 RT of the protein tyrosine kinase family";
 RL Gene 85:67-74 (1989).
 CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1 ALTERNATIVE PRODUCTS: 2 ISOFORMS, LYN A (SHOWN HERE) AND LYN B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1 TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND
 CC MYELOID CELLS.
 CC -1 SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1 SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1 SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 CC EMBL: M64608; AAA39470.1; -;
 CC EMBL: M57696; AAA39471.1; -;
 CC EMBL: M57697; AAA39472.1; -;
 CC EMBL: M33426; AAA40017.1; -;
 CC PIR: A39719; A39719.
 CC HSSP: P06631; 1ADS.
 CC MGD: MGI:96892; LYN.
 DR InterPro: IPR000719; Euk_kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00069; Kinase; 1.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_kinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SMO0252; SH2; 1.
 DR SMART: SMO0326; SH3; 1.
 DR SMART: SMO0219; TYKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00001; SH2; 1.
 DR PROSITE: PS00002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 FT INIT MET 0 BY SIMILARITY.
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 2 PALMITATE (BY SIMILARITY).
 FT DOMAIN 62 122 SH3.
 FT DOMAIN 128 225 SH2.
 FT DOMAIN 246 500 PROTEIN_KINASE.
 FT NP_BIND 252 260 ATP (BY SIMILARITY).
 FT BINDING 274 274 ATP (BY SIMILARITY).
 FT ACT_SITE 366 366 BY SIMILARITY.
 FT MOD_RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT MOD_RES 507 507 PHOSPHORYLATION (BY SIMILARITY).
 FT VARSPLIT 24 44 MISSING (IN ISOFORM LYN B).
 FT CONFLICT 76 76 I -> F (IN REF. 2).
 FT CONFLICT 160 160 L -> I (IN REF. 2).
 FT CONFLICT 278 278 P -> L (IN REF. 2).
 FT CONFLICT 390 390 V -> I (IN REF. 2).
 FT CONFLICT 414 414 I -> F (IN REF. 3).
 FT CONFLICT 424 424 D -> N (IN REF. 1).
 FT CONFLICT 431 431 L -> P (IN REF. 3).
 SQ SEQUENCE 511 AA; 58681 MW; 3935221CC90C5070 CRC64;
 Query Match 27.5%; Score 371.5; DB 1; Length 511;
 Best Local Similarity 40.8%; Pred. No. 3.2e-24;
 Matches 82; Conservative 33; Mismatches 77; Indels 9; Gaps 3;
 QY 6 SRRKSLPSSLSVGGQGVMTAEERKATVAALGSPAGPAELSLRGEPLTISED 65
 DB 37 SNKQRPVEF-HLPGQRFQTKDPEQGDIVALLPYDGHDDLSFKKGEKMYLEEH 95
 QY 66 GDMWTULSEVSGREYNIPSVHAKV---SHGMLYEGLSREKAEILLLPNGGAFILR 121
 DB 96 GEMWKAISLSKREGEFIPSNYAKVNTLETBEWFFDITRKDARQLAPGNSAGAFILR 155
 QY 122 ESQTRGYSLSVRLSRPASMDRIRHRIHCLDNGMLYISPRLTPEPLALVDHYSELAD 181
 DB 156 ESETLKSPFLSVRDYDPMHGDVHKYKISLNDGCIYIISPRITFPDISMTKHYQKSD 215
 QY 182 DICLLKEPCVLOKAGPLPK 202
 DB 216 GLCRRLERKACI---SPKPOK 232
 RESULT 3
 LYN_RAT STANDARD; PRT; 511 AA.
 AC Q07014; Q63320;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
 GN LYN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Minoguchi K., Nishikata H., Siraganian R.P.;
 RT "Bacterially expressed rat p56lyn binds several proteins in rat
 RT basophilic leukemia cells including pp72, a tyrosine phosphorylated
 RT protein prominent in activated cells.";
 RL J. Immunol. 150:222-222(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94171041; PubMed=8125304;
 RA Rider L.G., Raben N., Miller L., Jelsema C.;
 RT "The CDNA encoding two forms of the LYN protein tyrosine kinase are
 RT expressed in rat mast cells and human myeloid cells.";
 RL Gene 138:219-222 (1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97442484; PubMed=9295361;
 RA Vonakis B.M., Chen H., Haleem-Smith H., Metzger H.;
 RT "The unique domain as the site on LYN kinase for its constitutive
 RT association with the high affinity receptor for IgE.";
 RL J. Biol. Chem. 272:24072-24080(1997).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, LYN A (SHOWN HERE) AND LYN B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND
 CC MYELOID CELLS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC

CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 DR EMBL: L14951; AAA1549.1; -;
 DR EMBL: L14782; AAA20945.1; -;
 DR EMBL: L14823; AAA20945.1; -;
 DR EMBL: AF000300; AAB71344.1; -;
 DR EMBL: AF000301; AAB71345.1; -;
 DR EMBL: AF000302; AAB71346.1; -;
 DR HSSP: P08631; 1A05.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00325; SH3; 1.
 DR SMART: SM00219; TYKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferrase; ATP-binding; Myristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternating splicing.
 FT INIT_MET 0 0
 FT LIPID 1 1
 FT LIPID 2 2
 FT DOMAIN 62 122
 FT DOMAIN 128 225
 FT DOMAIN 246 500
 FT NP_BIND 252 260
 FT BINDING 274 274
 FT ACT_SITE 366 366
 FT MOD_RES 396 396
 FT MOD_RES 507 507
 FT MOD_RES 507 507
 FT VARSPLIT 24 44
 FT CONFLICT 230 230
 FT CONFLICT 307 307
 FT CONFLICT 418 418
 SQ SEQUENCE 511 AA; 58529 MW; 24A2B5E229CD43ED CRC64;
 Query Match 27.5%; Score 371.5; DB 1; Length 511;
 Best Local Similarity 40.8%; Pred. No. 3.2e-24;
 Matches 82; Conservative 33; Mismatches 77; Indels 9; Gaps 3;
 QY 6 SRRKSLPSSLSVGGQGVMTAEERKATVAALGSPAGPAELSLRGEPLTISED 65
 DB 37 SNKQRPVEF-HLPGQRFQTKDPEQGDIVALLPYDGHDDLSFKKGEKMYLEEH 95
 QY 66 GDMWTULSEVSGREYNIPSVHAKV---SHGMLYEGLSREKAEILLLPNGGAFILR 121
 DB 96 GEMWKAISLSKREGEFIPSNYAKVNTLETBEWFFDITRKDARQLAPGNSAGAFILR 155
 QY 122 ESQTRGYSLSVRLSRPASMDRIRHRIHCLDNGMLYISPRLTPEPLALVDHYSELAD 181

DB 156 ESETLKGSFSLVDYDPMHGVITKHYKIRSLDNGGYISPRITPCISDMIKHYKOSD 215
 OY 182 DICCLKEPCVLOPAGPLPCK 202
 DB 216 GICRLEKACI----SPKPK 232

RESULT 4
 ID_HCK_HUMAN STANDARD: PRT; 526 AA.
 AC P08631; O96CC0; O9HSY5; O9NUA4; Q9UMJ5;
 DT 01-AUG-1998 (Rel. 08, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (p59-HCK and p60-HCK)
 DE (Hemopoietic cell kinase).
 GN HCK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID:9606;
 RN [1]
 RP MEDLINE=87257942; PubMed=3496523;
 RA Quintrell N., Lebo R., Varmus H., Bishop J.M., Pattenati M.J.,
 le Beau M.M., Diaz M.O., Rowley J.D.;
 RT "Identification of a human gene (HCK) that encodes a protein-tyrosine
 RT kinase and is expressed in hemopoietic cells.";
 RL Mol. Cell. Biol. 7:2267-2275 (1987).
 RN [2]
 RP SEQUENCE OF 22-526 FROM N.A.
 RX MEDLINE=87257943; PubMed=3453117;
 RA Ziegler S.F., March J.D., Lewis D.B., Perlmutter R.M.;
 RT "Novel protein-tyrosine kinase gene (hck) preferentially expressed in
 RT cells of hematopoietic origin.";
 RL Mol. Cell. Biol. 7:2276-2285 (1987).
 RN [3]
 RP SEQUENCE OF 22-526 FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 22-526 FROM N.A.
 RC TISSUE=ileal mucosa;
 RA Kawakami T., Nouchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
 Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
 Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y., Ota T., Suzuki Y.,
 Otagashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
 Isegaki T., Sugano S.;
 RT "MEDO human cDNA sequencing project.";
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashworth J., Burton J., Gilbert J.G.R.,
 Jones M., Scavrides G., Almeida J.P., Babage A.K., Baguley C.L.,
 Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
 Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cordy N.R.,
 Coulson A., Coville G.J., Deadman R., Dhand P.D., Dunn M.,
 Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.U.,
 Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 Leharvalho M.H., Leverisa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,
 Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 Phillimore B.O.C.T., Prachalingam S.R., Plumb R.W., Ramsay H.,
 Rice C.M., Ross M.T., Scott C.E., Sehara H.K., Showken R., Sims S.,
 Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 Wilmink L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 Rogers J.,
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871 (2001).
 RN [6]
 RP SEQUENCE OF 179-526 FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=92241680; PubMed=1572549;
 RA Hradetzky D., Streibhardt K., Ruesamen-Waigmann H.;
 RT "The genomic locus of the human hemopoietic-specific cell protein
 RT tyrosine kinase (PTK)-encoding gene (HCK) confirms conservation of
 RT exon-intron structure among human PTKs of the src family.";
 RL Gene 113:275-280 (1992).
 RN [7]
 RP SEQUENCE OF 1-22 FROM N.A., AND ALTERNATIVE INITIATION.
 RX MEDLINE=91342636; PubMed=1875927;
 RA Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Dunn A.R.;
 RT "Two isoforms of murine hck, generated by utilization of alternative
 RT translational initiation codons, exhibit different patterns of
 RT subcellular localization.";
 RL Mol. Cell. Biol. 11:4363-4370 (1991).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 78-526.
 RX MEDLINE=9717106; PubMed=9024658;
 RA Sichert F., Moarefi I., Kuriyan J.;
 RT "Crystal structure of the Src family tyrosine kinase Hck.";
 RL Nature 385:602-609 (1997).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 81-137.
 RX MEDLINE=98453315; PubMed=9778343;
 RA Arold S., O'Brien R., Franken P., Strub M.P., Hoh F., Dumas C.,
 Ladbury J.E.;
 RT "RT loop flexibility enhances the specificity of Src family SH3
 RT domains for HIV-1 Nef.";
 RL Biochemistry 37:14683-14691 (1998).
 RN [10]
 RP STRUCTURE BY NMR OF 78-138.
 RX MEDLINE=98239731; PubMed=9571048;
 RA Horita D.A., Baldisseri D.M., Zhang W., Alteri A.S., Smithgall T.E.,
 Greiner W.H., Byrd R.A.;
 RT "Solution structure of the human Hck SH3 domain and identification of
 RT its ligand binding site.";
 RL J. Mol. Biol. 278:253-265 (1998).
 RN [11]
 RP STRUCTURE BY NMR OF 139-245.
 RX MEDLINE=97263487; PubMed=9109402;
 RA Zhang W., Smithgall T.E., Greiner W.H.;
 RT "Sequential assignment and secondary structure determination for the
 RT Src homology 2 domain of hematopoietic cellular kinase.";
 RL FEBS Lett. 406:131-135 (1997).
 RN [12]
 RP RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
 RP CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 RP DEGRADATION OF NEUTROPHILS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: p60-HCK AND p59-HCK ARE ASSOCIATED WITH
 CC MEMBRANES. p60-HCK IS ALSO CYTOPLASMIC (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; p60-HCK (shown here) and p59-
 CC HCK; are produced by alternative initiation.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE
 CC MYELOID AND B-LYMPHOID LINEAGES.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@lsb-sib.ch).

CC EMBL, M16591; AAA52643.1; -
DR EMBL, M16592; AAA52644.1; -
DR EMBL, BC014435; AAH14435.1; -
DR EMBL, AK026432; BAB15482.1; -
DR EMBL, AL049539; CAB75606.1; -
DR EMBL, X58741; CAA41565.2; -
DR EMBL, X58742; CAA41565.2; JOINED.
DR EMBL, X58743; CAA41565.2; JOINED.
DR FIR, A27812; TYHHC.
DR PDB, 2HCK; 20-AUG-97.
DR PDB, 3HCK; 15-OCT-97.
DR PDB, 4HCK; 17-JUN-98.
DR PDB, 5HCK; 17-JUN-98.
DR PDB, 1AD5; 15-MAY-97.
DR PDB, 1BU1; 11-NOV-98.
DR Genew; HGNC:4840; HCK.
DR MIM, 142370; -
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR Pfam; PF00069; Pkinase; 4.
DR ProDom; PD000065; SH3; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00002; SH2; 1.
DR PROSITE; PS00001; SH3; 1.
DR Transferrase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
KW Myristate; SH2 domain; SH3 domain; Alternative initiation;
KW 3D-structure.
FT CHAIN 1 526 TYROSINE-PROTEIN KINASE P59-HCK.
FT CHAIN 22 526 TYROSINE-PROTEIN KINASE P59-HCK.
FT INIT MET 22 22 FOR ISOFORM P59-HCK.
FT DOMAIN 78 138 SH3.
FT DOMAIN 144 241 SH2.
FT NP_BIND 262 515 PROTEIN KINASE.
FT BINDING 268 276 ATP.
FT ACT SITE 290 290 ATP.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
FT LIPID 23 23 MYRISTATE (BY SIMILARITY).
FT MOD_RES 411 411 C -> S (IN REF. 1).
FT CONFLICT 24 24 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CONFLICT 144 144 W -> R (IN REF. 4).
SQ SEQUENCE 526 AA; 59539 MW; 8478877A0A641725 CRC64;
Query Match 27.0%; Score 364.5; DB 1; Length 526;
Best Local Similarity 42.2%; Pred. No. 1.3e-23;
Matches 78; Conservative 31; Mismatches 69; Indels 7; Gaps 2;

QY 128 GSYLSVRLSPASWDRIHRYRTHCLDNGMVLISRLTPSLQALVDHSELDICLL 187
DB 178 GSYLSVRLSPASWDRIHRYRTHCLDNGMVLISRLTPSLQALVDHSELDICLL 237
QY 188 KPCV 192
DB 238 SVPCM 242
RESULT 5
HCK_MACFA STANDARD; PRT; 504 AA.
ID HCK MACFA
AC 095M30; (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase HCK (EC 2.7.1.12) (P56-HCK) (Hemopoietic cell
kinase).
DE HCK.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Picard C.;
RL Thesis (2001), University of Marseille, France.
CC - FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
CC DEGRADATION PROCESS OF NEUTROPHILS (By similarity).
CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC - SUBCELLULAR LOCATION: Membrane-associated (By similarity).
CC - SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC - SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC - SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@lsb-sib.ch).

CC EMBL, AJ320181; CAC44031.1; -
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000065; SH3; 1.
DR ProDom; PD000093; SH2; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00002; SH2; 1.
DR PROSITE; PS00001; SH3; 1.
DR Transferrase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
KW Myristate; SH2 domain; SH3 domain.
FT CHAIN 1 526 TYROSINE-PROTEIN KINASE P59-HCK.
FT CHAIN 22 526 TYROSINE-PROTEIN KINASE P59-HCK.
FT INIT MET 22 22 FOR ISOFORM P59-HCK.
FT DOMAIN 78 138 SH3.
FT DOMAIN 144 241 SH2.
FT NP_BIND 262 515 PROTEIN KINASE.
FT BINDING 268 276 ATP.
FT ACT SITE 290 290 ATP.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
FT LIPID 23 23 MYRISTATE (BY SIMILARITY).

FT MOD RES 389 389 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 504 AA; 57096 MW; 53B29322D2DE3423 CRC64;
 Query Match
 Best Local Similarity 26.8%; Score 362; DB 1; Length 504;
 Matches 73; Conservative 29; Mismatches 53; Indels 4; Gaps 1;
 QY 38 VALGSPAGPAELSLRLGEPITVSEDDGMWTVLSEVSGREXNIPSVHAKV-----SHG 93
 DB 62 VALYDEAIHEDLSFGKQGVVLEESGEMWKARSLATKEGYPISVYVARVDSLETET 121
 QY 94 WLYEGLSRKAEELLPGNPGAPFLRESQTRGGSYSLSVRLSPASWDRIRHYRHL 153
 DB 122 WPKGSRKDAERHLAPGMGLSPWIDSETTGSGYSLSVVDYDPOGDTVKYKIRTL 181
 QY 154 DNGWLTSPRLTSPSLQALVDHYSELADICCLKEPCV 192
 DB 182 DNGEYISPRSTFSTLQELVHYKKGSDGLCKLSPVCV 220
 RESULT 6
 HCK_RAT STANDARD; PRT; 503 AA.
 AC P50545; O64647;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P50-HCK) (hemopoietic cell kinase).
 GN HCK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 ON NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92109719; PubMed=1764064;
 RA Okano Y., Sugimoto Y., Fukuoka M., Matsui A., Nagata K.I., Nozawa Y.;
 RT "Identification of rat cDNA encoding hck tyrosine kinase from megakaryocytes";
 RL Biochem. Biophys. Res. Commun. 181:1137-1144(1991).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Spleen;
 RA Vijaya Gouri B.S., Renu V., Kamatkar S., Swarup G.;
 RT "Nucleotide sequence of a cDNA coding for rat hck tyrosine kinase and characterization of its gene product";
 RL J. Biocel. 19:117-129(1994).
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE DEGRANULATION PROCESS OF NEUTROPHILS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC EMBL: S74141; AA020754.1; -;
 CC EMBL: M83666; AAA41312.1; -;
 CC EMBL: X62345; AAA44218.1; -;
 CC HSPSP; P08631; IBI1.
 DR Interpro; IPR000719; Euk_pkinase.

DR Interpro; IPR000980; SH2.
 DR Interpro; IPR001452; SH3.
 DR Interpro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00319; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Transferase; Tyrosine-protein kinase; phosphorylation; ATP-binding;
 KM Myristate; SH2 domain; SH3 domain.
 FT DOMAIN 55 115
 FT DOMAIN 121 216
 FT DOMAIN 239 492
 FT NP_BIND 245 253
 FT BINDING 267 267
 FT ACT_SITE 358 358
 FT LIPID 2 2
 FT MOD_RES 388 388
 FT CONFLICT 51 51
 FT CONFLICT 205 205
 FT CONFLICT 306 306
 SQ SEQUENCE 503 AA; 57016 MW; 57016 MW; A1CF13F0E82F73 CRC64;
 Query Match
 Best Local Similarity 37.6%; Pred. No. 4.9e-23;
 Matches 86; Conservative 36; Mismatches 76; Indels 31; Gaps 5;
 QY 1 MGSLSR-RKSLPSPSSVCGGQPYTME-----AESKAT-A 37
 DB 1 MGVKSRFLRSGSKSKIEPRANQGPVVPDPPTSPKGLCPNSINSLPRGVESEDTIV 60
 QY 38 VALGSPAGPAELSLRLGEPITVSEDDGMWTVLSEVSGREXNIPSVHAKV-----SHG 93
 DB 61 VALYDEAIHEDLSFGKQGVVLEESGEMWKARSLATKEGYPISVYVARVDSLETET 120
 QY 94 WLYEGLSRKAEELLPGNPGAPFLRESQTRGGSYSLSVRLSPASWDRIRHYRHL 153
 DB 121 WPKGSRKDAERHLAPGMGLSPWIDSETTGSGYSLSVVDYDPOGDTVKYKIRTL 180
 QY 154 DNGWLTSPRLTSPSLQALVDHYSELADICCLKEPCVLRAGLPCK 202
 DB 181 DSGEYISPRSTFSTLQELVHYKKGSDGLCKLSPVCV-----SPKPK 225
 RESULT 7
 BLK_HUMAN STANDARD; PRT; 504 AA.
 ID BLK_HUMAN
 AC P51451; Q16291;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase BLK (EC 2.7.1.112) (B lymphocyte kinase) (p55-BLK).
 GN BLK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95123078; PubMed=7822795;

RA Islem K.B., Rabbani H., Larsson C., Sanders R., Smith C.I.
 RT "Molecular cloning, characterization, and chromosomal localization of
 RT a human lymphoid tyrosine kinase related to murine Btk."
 RL J. Immunol. 154:1265-1272(1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95148218; PubMed=7845672;
 RA Drebin J.A., Hartzell S.W., Griffin C., Campbell M.J.,
 RA Niederhuber J.E.;
 RT "Molecular cloning and chromosomal localization of the human homologue
 RT of a B-lymphocyte specific protein tyrosine kinase (btk)."
 RL Oncogene 10:477-486(1995).
 CC -1- FUNCTION: BTK MAY FUNCTION IN A SIGNAL TRANSDUCTION PATHWAY THAT
 CC IS RESTRICTED TO B LYMPHOID CELLS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTRAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTRAINS 1 SH3 DOMAIN.
 CC -----
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 CC or send an email to license@isb-sdb.ch).
 CC -----
 DR EMBL, 23198; CAAB3965.1; -;
 DR EMBL, 576617; AAB31265.1; -;
 DR HSSP, P16277; BLK.
 DR Genew, HGNC:1057; BLK.
 DR MIM, 191305; -;
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001452; Tyr_Pkinase.
 DR Pfam, PF00017; SH2; 1.
 DR Pfam, PF00018; SH3; 1.
 DR Pfam, PF00069; Pkinase; 1.
 DR PRINTS, PRO0401; SH2DOMAIN.
 DR PRINTS, PRO0452; SH3DOMAIN.
 DR PRINTS, PRO0109; TYRKINASE.
 DR ProDom, PD000001; Euk_Pkinase; 1.
 DR ProDom, PD000066; SH3; 1.
 DR ProDom, PD000093; SH2; 1.
 DR SMART, SM00252; SH2; 1.
 DR SMART, SM00326; SH3; 1.
 DR SMART, SM00219; Tyrc; 1.
 DR PROSITE, PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE, PS00109; PROTEIN KINASE TYR; FALSE_NEG.
 DR PROSITE, PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE, PS00011; SH2; 1.
 DR PROSITE, PS00002; SH3; 1.
 DR Tyrosine-protein kinase; Phosphorylation; Transferase; ATP-binding;
 KM Myristate; SH2 domain; SH3 domain.
 FT INIT MET 0
 FT LIPID 0
 FT DOMAIN 1 1 MYRISTATE (BY SIMILARITY).
 FT DOMAIN 57 117 SH3.
 FT DOMAIN 123 219 SH2.
 FT DOMAIN 240 493 PROTEIN KINASE.
 FT NP_BIND 246 254 ATP (BY SIMILARITY).
 FT BINDING 268 268 ATP (BY SIMILARITY).
 FT ACT_SITE 359 359 BY SIMILARITY.
 FT MOD_RES 388 388 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CONFLICT 286 286 M -> V (IN REF. 2).
 FT CONFLICT 406 406 I -> Y (IN REF. 2).
 SQ SEQUENCE 504 AA; 57607 MW; BDDIDP50C7370C8 CRC64;

Query Match 26.4%; Score 356.5; DB 1; Length 504;
 Best Local Similarity 44.2%; Pred. No. 6e-23;
 Matches 76; Conservative 24; Mismatches 67; Indels 5; Gaps 2;

 QY 25 PVTMEARESKATVALGSPFAGGPAELSLRLGEPITVSDGDMWTVLSEVSGREYVPS 84
 DB 50 PPDEHLEDDKHFFVALLDYLTAMNDRDLQMLKGEKQLVLTGKGDMVLAFLVYTGREGVPS 109
 QY 85 VHVAKVS---HGMYEGLSEKXAEELLILLPNNPGGAFILRESQTRGYSYLSRSLRPA 140
 DB 110 NFAVARESLSEMRWFFRSGQKREARQLAPINAKGSFLRESLTKGAFSLVAK-DVTT 168
 QY 141 SWDIRHYRHLNDGMYLISPLTPPSLQALVDHYSELADICLLKEPCV 192
 DB 169 QGELIKHYKRIQDEGGYISPIRTPPSLQALVHYSEKKGDCQRLTLPV 220
 RESULT 8
 HCK_MOUSE
 ID HCK_MOUSE STANDARD; PRT; 524 AA.
 AC P08103;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK and P60-HCK)
 GN (Hemopoietic cell kinase) (B-cell/myeloid kinase) (BHK).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 22-524 FROM N.A.
 RC STRAIN=ICR; TISSUE=Macrophage;
 RX MEDLINE=88067781; PubMed=3684607;
 RA Klemz M.J., McKercher S.R., Maki R.A.;
 RT "Nucleotide sequence of the mouse hck gene";
 RL Nucleic Acids Res. 15:9600-9600(1987).
 RN [2]
 RP SEQUENCE OF 22-524 FROM N.A.
 RX MEDLINE=88068587; PubMed=3317404;
 RA Holtzman D.A., Cook W.D., Dunn A.R.;
 RT "Isolation and sequence of a cDNA corresponding to a src-related gene
 RT expressed in murine hemopoietic cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8325-8329(1987).
 RN [3]
 RP SEQUENCE OF 1-22 FROM N.A., AND ALTERNATIVE INITIATION.
 RX MEDLINE=9142636; PubMed=1875927;
 RA Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Dunn A.R.;
 RT "Two isoforms of murine hck, generated by utilization of alternative
 RT translational initiation codons, exhibit different patterns of
 RT subcellular localization";
 RL Mol. Cell. Biol. 11:4363-4370(1991).
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 CC DEGRANULATION PROCESS OF NEUTROPHILS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: P59-HCK AND P56-HCK ARE ASSOCIATED WITH
 CC MEMBRANES. P59-HCK IS ALSO CYTOPLASMIC.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: IP59-HCK (shown here) and P56-
 CC HCK; are produced by alternative initiation.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE
 CC MYELOID AND B-LYMPHOID LINEAGES.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTRAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTRAINS 1 SH3 DOMAIN.
 CC -----
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FT BINDING 262 262 ATP (BY SIMILARITY).
 FT ACT SITE 353 353 BY SIMILARITY.
 FT MOD RES 382 382 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 498 AA; 56513 MW; BE49D7B079FDD577 CRC64;

Query Match 25.6%; Score 345.5; DB 1; Length 498;
 Best Local Similarity 40.5%; Pred. No. 5.1e-22;
 Matches 75; Conservative 29; Mismatches 64; Indels 17; Gaps 3;

QY 12 PPSPLSSVGGQPTVMERSKATNVALGSPAGAPAEISLRIGEPITLVSEDDQMTV 71
 DB 43 PSEN-----QDDDEERFVALFDYNAVNDRLQVLGKQLQVLSSTDWMLA 90
 QY 72 LSEVSGREYNIPIVHVAKVS----HGLVLEGLSRKAEELLPLPGNGAFILRESQTR 127
 DB 91 RSLVTGREGVPSNFPVAPVETLEVKKWFPRTISRKDAERQGLAPMNAKGSFILRESSENK 150
 QY 128 GSVLSVRLSRPASMDRIKRIHICLNGMLYISRLTFLPSLQLVHNSLADICLL 187
 DB 151 GAFSLSVK-DITTOGEVVAHKIKSLNLSGYSIPRTTPTLQALVQHSKXGDLCKQL 209
 QY 188 KPCV 192
 DB 210 TLPCV 214

RESULT 10

LC_HUMAN
 ID LC_HUMAN STANDARD; PRT; 508 AA.
 AC P06239; P07100; Q9NYT8; Q96DM4; Q13152; Q12850;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (556-LCK)
 DE (LCK) (T cell-specific protein-tyrosine kinase).
 GN LCK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89123626; PubMed=2265417;
 RA Perlmutter R.M., March J.D., Lewis D.B., Peet R., Ziegler S.F.,
 RA Wilson C.B.;
 RT "Structure and expression of lck transcripts in human lymphoid
 RT cells.";
 RL J. Cell. Biochem. 38:117-126(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87133831; PubMed=3493153;
 RA Koga Y., Caecia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
 RA Mak T.W.;
 RT "A human T cell-specific cDNA clone (YT16) encodes a protein with
 RT extensive homology to a family of protein-tyrosine kinases.";
 RL Eur. J. Immunol. 16:1643-1646(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90108697; PubMed=255056;
 RA Rorer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
 RA Benarous R.;
 RT "Structure of the human lck gene: differences in genomic organisation
 RT within src-related genes affect only N-terminal exons.";
 RL Gene 84:105-113(1989).
 RN [4]
 RP SEQUENCE FROM N.A.; VARIANTS L-27; POKP-231 INS; V-352, L-446, AND
 RP PHOSPHORYLATION OF TYR-393 AND TYR-504.
 RC TISSUE=Leukemia;
 RX MEDLINE=94187714; PubMed=8135546;
 RA Wright D.D., Setton B.W., Kampa M.P.;
 RT "Oncogenic activation of the lck protein accompanies translocation of
 RT the lck gene in the human HSB2 T-cell leukemia.";
 RL Mol. Cell. Biol. 14:2429-2437(1994).

RN [5]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Leukemic T-cell;
 RX MEDLINE=96085119; PubMed=7495859;
 RA Vogel L.B., Arthur R., Fujita D.J.;
 RT "An aberrant lck mRNA in two human T-cell lines.";
 RL Biochim. Biophys. Acta 1264:168-172(1995).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 13-508 FROM N.A.
 RC TISSUE=Peripheral blood lymphocytes;
 RX MEDLINE=20462621; PubMed=11009097;
 RA Borcistano W., Mayolini W.B., D'Elia M.M., Pacini S., Valensin S.,
 RA Olivieri C., Amadei A., Falini B., Del Prete G., Telford J.L.,
 RA Baldari C.T.;
 RT "Defective recruitment and activation of ZAP-70 in common variable
 RT immunodeficiency patients with T cell defects.";
 RL Eur. J. Immunol. 30:2632-2638(2000).
 RN [8]
 RP SEQUENCE OF 367-508 FROM N.A.
 RX MEDLINE=88217332; PubMed=2835736;
 RA Veilleux A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.;
 RT "Expression of the lck tyrosine kinase gene in human colon carcinoma
 RT and other non-lymphoid human tumor cell lines.";
 RL Oncogene Res. 1:357-374(1987).
 RN [9]
 RP SEQUENCE OF 374-508 FROM N.A.
 RX MEDLINE=87000726; PubMed=3489486;
 RA Treviñ J.M., Lin Y., Chen S.D., Phillips C.A., Canna C.,
 RA Lima T.J.;
 RT "Human T lymphocytes express a protein-tyrosine kinase homologous to
 RT p56LCK.";
 RL Biochim. Biophys. Acta 888:286-295(1986).
 RN [10]
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=89096891; PubMed=2850479;
 RA Garvin A.M., Pawar S., March J.D., Perlmutter R.M.;
 RT "Structure of the murine lck gene and its rearrangement in a murine
 RT lymphoma cell line.";
 RL Mol. Cell. Biol. 8:3058-3064(1988).
 RN [11]
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=89313764; PubMed=2787474;
 RA Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
 RA Miyamoto N.G., Mak T.W.;
 RT "Structure of the two promoters of the human lck gene: differential
 RT accumulation of two classes of lck transcripts in T cells.";
 RL Mol. Cell. Biol. 9:2173-2180(1989).
 RN [12]
 RP MASS SPECTROMETRY.
 RC TISSUE=Breast cancer;
 RX MEDLINE=21829512; PubMed=11840567;
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
 RA Ferehn R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
 RA Zvelebil M.J.;
 RT "Cluster analysis of an extensive human breast cancer cell line
 RT protein expression map database.";
 RL Proteomics 2:212-223(2002).
 RN [13]
 RP INTERACTION WITH PI3K.
 RX MEDLINE=94067101; PubMed=7504174;
 RA Vogel L.B., Fujita D.J.;
 RT "The SH3 domain of p56lck is involved in binding to
 RT phosphatidylinositol 3'-kinase from T lymphocytes.";
 RL Mol. Cell. Biol. 13:7408-7417(1993).
 RN [14]
 RP INTERACTION WITH KHDRBS1.
 RX MEDLINE=95155308; PubMed=7852312;
 RA Vogel L.B., Fujita D.J.;

Db 211 ASDGLCTKLRPCQTOK 227

RESULT 12

LCK CHICK STANDARD; PRT; 507 AA.

AC P42683;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK (EC 2.7.1.112) (Protein-tyrosine kinase C-TKL).

GN LCK.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI_TaxID=9031.

OX [1]

RN [1]

RP SEQUENCE OF 1-88 FROM N.A.

RX MEDLINE=9218685; PubMed=1545804;

RA Chow L., Ratcliffe M., Veilleux A.;

RT "tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene.";

RL Mol. Cell. Biol. 12:1226-1233(1992).

RN [2]

RP SEQUENCE OF 46-507 FROM N.A.

RX MEDLINE=88097370; PubMed=3321053;

RA Strehnard K., Mullins J.I., Bruck C., Ruebamen-Waigmann H.;

RT "Additional member of the protein-tyrosine kinase family: the src- and lck-related protooncogene c-tkl.";

RL Proc. Natl. Acad. Sci. U.S.A. 84:8778-8782(1987).

CC -1- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER CDA OR CD8.

CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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CC EMBL; M85043; AAA49003.1; -

DR EMBL; J03579; AAA49081.1; ALU_INIT.

DR HSSP; P06239; 3LCK.

DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR000980; SH2.

DR InterPro; IPR001452; SH3.

DR InterPro; IPR001451; Tyr_kinase.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 1.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00452; SH3DOMAIN.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Euk_pkinase; 1.

DR ProDom; PD000066; SH3; 1.

DR ProDom; PD000093; SH2; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 1.

DR SMART; SM00219; TyKc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS50001; SH2; 1.

DR PROSITE; PS50002; SH3; 1.

KW PROTO-ONCOGENE; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION; TRANSFERASE;

KW ATP-BINDING; MYRISTATE; SH2 DOMAIN; SH3 DOMAIN; PALMITATE;

KW Lipoprotein.

FT INT MET 0 0 PROBABLE.

FT LIPID 1 1 MYRISTATE (BY SIMILARITY).

FT LIPID 2 2 PALMITATE (BY SIMILARITY).

FT LIPID 4 4 PALMITATE (BY SIMILARITY).

FT LIPID 59 119 SH3.

FT DOMAIN 125 222 SH2.

FT DOMAIN 125 222 SH2.

FT DOMAIN 243 496 PROTEIN KINASE.

FT NP BIND 249 257 ATP (BY SIMILARITY).

FT BINDING 271 271 ATP (BY SIMILARITY).

FT ACT SITE 362 362 BY SIMILARITY.

FT MOD_RES 392 392 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT MOD_RES 503 503 PHOSPHORYLATION (NEGATIVE REGULATION) (BY SIMILARITY).

FT SQ SEQUENCE 507 AA; 58008 MW; BC93C4FA891B6170 CRC64;

Query Match 24.9%; Score 337; DB 1; Length 507;

Best Local Similarity 43.8%; Pred. No. 2.8e-21;

Matches 71; Conservative 27; Mismatches 60; Indels 4; Gaps 1;

QY 38 VALSPAGAPAEISLRGEPLTIVSPDGMWTVLSVSGREYNISVHAKVS---HG 93

DB 65 VALDYEPPTHDGLGKQEKRLRVLESGBMRAOSLTGEGLIHNFVAVNLSLEPEP 124

QY 94 WLVEGLSREKAEELLPLPGNPGAFILRESQTRGYSVLSVRPASPMDIRIRHICL 153

DB 125 WFFNKLNRKVAERILIASGNTHGSFLLRESETSKGSYSLSVPDQNOGETVKAHYKINM 184

QY 154 DNGMLYSPRLTPSPCALVNDYSELADIDCLLKEPVLOR 195

DB 185 DNGGYISPRVTFSSLHVEIVYSSSDGLCTRLEKPCRTOK 226

RESULT 13

YES_XENLA STANDARD; PRT; 537 AA.

ID YES_XENLA

AC P10536;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112) (661-YES) (C-YES).

DE (C-YES).

GN YES.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OC NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89296347; PubMed=2472592;

RA Steele R.E., Irwin M.Y., Knudsen C.L., Collett J.W., Fero J.B.;

RT "The yes proto-oncogene is present in amphibians and contributes to the maternal RNA pool in the oocyte.";

RL Oncogene Res. 4:223-233(1989).

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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DR EMBL: X14377; CAA32551.1; -
 DR PIR: S08517; S08517.
 DR HSP: P00523; 2PTK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00109; PROTEIN KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR Proto-oncogene: Tyrosine-protein kinase; Phosphorylation;
 KW Transferase; ATP-binding; Myristate; SH3 domain; SH2 domain.
 FT LIPID 2
 FT DOMAIN 85 146 SH3.
 FT DOMAIN 152 249 SH2.
 FT DOMAIN 271 524 PROTEIN KINASE.
 FT NP_BIND 277 285 ATP (BY SIMILARITY).
 FT BINDING 299 299 ATP (BY SIMILARITY).
 FT ACT_SITE 390 390 BY SIMILARITY.
 FT MOD_RES 420 420 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 537 AA; 60357 MW; P26F615940AC1B CRC64;

Query Match 23.9%; Score 323.5; DB 1; Length 537;
 Best Local Similarity 33.6%; Pred. No. 4.3e-20;
 Matches 85; Conservative 38; Mismatches 91; Indels 39; Gaps 7;

Qy 38 VALGSPAGPAELSLRGEPLTIVE-DGDMWTVLSEVGREYNIPSVHAKV-----SH 92
 Db 91 VALDYDEARTTDSFRGSEFQIINNTGDMWEMRSATKTKGYIPSYVAPADSIQAE 150
 Qy 93 GMLYEGLSREKAEELLIPGPGAPLIESOTRRGYSISVLSPPASWDRIR-----H 147
 Db 151 EWFYGRGKRAERLLNPGNGRTFLVSESETTGAYSLISIR-----DWDENVGDMVKH 205
 Qy 148 YRIHCLDNGMLYISPLTSPSLQALVDHYSELADICCLKEPC-----VLORAGP 198
 Db 206 YKIRKLDNGGYITTRAFQESLQKLVKHSSEHAGDCYRLTYVCPVKPQTQGLAKDWE 265
 Qy 199 LPRGDIPLPYTVQR-----TPLNKVELDSLLFSEAAATGSESLSEGLRES 244
 Db 266 IPRESLRIDVKLGGCCFGEWVGWTNGTITKVAIKTLKRGTMPEAFIQAOIMKMLHDK 325
 Qy 245 L-SFYISLDEAV 256
 Db 326 LVPLVAIVSEEP 338

RESULT 14
 YES_CHICK
 ID YES_CHICK STANDARD; PRI: 541 AA.
 AC P09324;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase YES (EC 2.7.1.112) (P61-YES)
 DE (C-YES).
 GN YES.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=89041591; Pubmed=3054816;
 CC RA Sudol M., Kiewietter C., Zhao Y.H., Dorai T., Wang L.H.,
 CC Hanafusa H.,
 CC "Nucleotide sequence of a cDNA for the chick yes proto-oncogene:
 CC comparison with the viral yes gene."
 CC Nucleic Acids Res. 16:9876-9876(1988).
 CC [2]
 CC REVISION TO 232.
 CC Submitted (NOV-1988) to the EMBL/GenBank/DBJ databases.
 CC [3]
 CC SEQUENCE FROM N.A.
 CC TISSUE=Kidney, and Brain.
 CC MEDLINE=93096482; Pubmed=1281306;
 CC RA Marcelle C., Eichmann A.
 CC "Molecular cloning of a family of protein kinase genes expressed in
 CC the avian embryo."
 CC Oncogene 7:2479-2487(1992).
 CC [4]
 CC SEQUENCE OF 396-451 FROM N.A.
 CC MEDLINE=93096482; Pubmed=1281306;
 CC RA Marcelle C., Eichmann A.
 CC "Molecular cloning of a family of protein kinase genes expressed in
 CC the avian embryo."
 CC Oncogene 7:2479-2487(1992).
 CC [5]
 CC CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC [6]
 CC SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC [7]
 CC SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC [8]
 CC SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC [9]
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 CC or send an email to license@ebi.ac.uk).

FT DOMAIN 89 150 SH3.
 FT DOMAIN 156 253 SH2.
 FT DOMAIN 275 528 PROTEIN KINASE.
 FT NP_BIND 281 289 ATP (BY SIMILARITY).
 FT BINDING 303 303 ATP (BY SIMILARITY).
 FT ACT_SITE 394 394 BY SIMILARITY.
 FT MOD_RES 424 424 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CONFLICT 67 71 TPRFG -> IHELR (IN REF. 3).
 FT CONFLICT 82 82 P -> O (IN REF. 3).
 SQ SEQUENCE 541 AA: 60792 MW: 668496 CDD1755NAF CRC64;
 Query Match 23.8%; Score 321; DB 1; Length 541;
 Best Local Similarity 31.8%; Pred. No. 7, 1e-20;
 Matches 92; Conservative 43; Mismatches 104; Indels 50; Gaps 9;
 QY 2 GSPRRKSLPSPLSSVQGGPYTWAEARSKATYVALGSPFAGPAELSLRLGPLETL 61
 DB 70 GGASSPFAVSPSPSTLT---GQVTV-----FVALYDEARTDDLSFKGERRQI 118
 QY 62 VSE-DGDMWTVLSEVSGREYINIPSYHVAKV---SHGMLYEGLSREKAEELLRLPGRG 116
 DB 119 INNTEGDWWEARSLATGKTGYIPSNVYAPADSIQAEEMVFGKMGKDAERLLINPGRG 178
 QY 117 APFLRESQTRGYSLSVLRSPASMDRIR---HYRIHCLDNGMLYISPRLTSPSLQA 171
 DB 179 IFVASEETTKGAVSLIR-----DMDEVGDNVKKYKIRKLDNGGYITTRAQFESLQK 233
 QY 172 LVDRSELDIDICCLKEPC-----VLQRAGLPFGKDIPLPYTVQR----- 212
 DB 234 LVKHYREHADGLCHKLTTCPTVKEPQTQGLAKDAMEIPRESLRLEVKLQGCCEVWMT 293
 QY 213 ----TPLNKKELDSLLFSBAATGESLSEGLRESL-SFYISLNDENV 256
 DB 294 WNGTKKVAIKTLKGTWMEAPFLQAOIMKKLRHDKVLPLVAVVEEPI 342
 RESULT 15
 FYN_HUMAN STANDARD; PRT; 536 AA.
 AC P06241;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2003 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase FYN (EC 2.7.1.112) (P59-FYN)
 GN FYN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RK MEDLINE=86287278; PubMed=3526330;
 RA Samba K., Nishizawa M., Miyajima N., Yoshida M.C., Sukegawa J.,
 RA Yamashita Y., Sasaki M., Yamamoto T., Toyoshima K.;
 RT "Yes-related protooncogene, *lyn*, belongs to the protein-tyrosine
 RT kinase family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5459-5463 (1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RK MEDLINE=87089775; PubMed=3099169;
 RA Kawakami T., Pennington C.Y., Robbins K.C.;
 RT "Isolation and oncogenic potential of a novel human *src*-like gene.";
 RL Mol. Cell. Biol. 6:4195-4201 (1986).
 RN [3]
 RP MYRISTOYLATION, AND PHOSPHORYLATION OF TYR-530.
 RX MEDLINE=91016431; PubMed=1699196;
 RA Peters D.J., McGrew B.R., Petron D.C., Lipcak L.M., Laudano A.P.;
 RT "In vivo phosphorylation and membrane association of the *fyn* proto-
 RT oncogene product in IM-9 human lymphoblasts.";
 RL Oncogene 5:1313-1319 (1990).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF SH3 DOMAIN.

RX MEDLINE=93327750; PubMed=7687536;
 RA Noble M.E.M., Musacchio A., Saraste M., Courtneidge S.A.,
 RA Wiernga R.K.;
 RT "Crystal structure of the SH3 domain in human Fyn; comparison of the
 RT three-dimensional structures of SH3 domains in tyrosine kinases and
 RT spectrin.";
 RL EMBO J. 12:2617-2624 (1993).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 80-141.
 RX MEDLINE=95393198; PubMed=7664083;
 RA Musacchio A., Saraste M., Williams M.;
 RT "High-resolution crystal structures of tyrosine kinase SH3 domains
 RT complexed with proline-rich peptides.";
 RL Nat. Struct. Biol. 1:546-551 (1994).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 84-140 IN COMPLEX WITH NEF.
 RX MEDLINE=96279837; PubMed=8681387;
 RA Lee C.H., Sakela K., Mirza U.A., Chait B.T., Kurlyan J.;
 RT "Crystal structure of the conserved core of HIV-1 Nef complexed with
 RT a *src* family SH3 domain.";
 RL Cell 85:931-942 (1996).
 RN [7]
 RP STRUCTURE BY NMR OF SH3 DOMAIN.
 RX MEDLINE=9639716; PubMed=8805554;
 RA Morton C.J., Pugh D.J.R., Brown E.L.J., Kahmann J.D., Renzoni D.A.C.,
 RA Campbell I.D.;
 RT "Solution structure and peptide binding of the SH3 domain from human
 RT Fyn.";
 RL Structure 4:705-714 (1996).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=9711261; PubMed=8961927;
 RA Renzoni D.A., Pugh D.J., Siliard G., Das P., Morton C.J., Rossi C.,
 RA Waterfield M.D., Campbell I.D., Ladbury J.E.;
 RT "Structural and thermodynamic characterization of the interaction of
 RT the SH3 domain from Fyn with the proline-rich binding site on the p85
 RT subunit of PI3-kinase.";
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 RP STRUCTURE BY NMR OF SH2 DOMAIN.
 RX MEDLINE=9803454; PubMed=9351806;
 RA Mulhern T.D., Shaw G.L., Morton C.J., Day A.J., Campbell I.D.;
 RT "The SH2 domain from the tyrosine kinase Fyn in complex with a
 RT phosphotyrosyl peptide reveals insights into domain stability and
 RT binding specificity.";
 RL Structure 5:1313-1323 (1997).
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 RP BINDING OF SH3 DOMAIN TO PI 3-KINASE.
 RX MEDLINE=99348274; PubMed=8394019;
 RA Prasad K.V., Janssen O., Kapeller R., Raab M., Cantley L.C.,
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 RT "Src-homology 3 domain of protein kinase p59fyn mediates binding to
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 RL Proc. Natl. Acad. Sci. U.S.A. 90:7366-7370 (1993).
 CC -1- FUNCTION: IMPLICATED IN THE CONTROL OF CELL GROWTH.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate. THROUGH ITS SH3 DOMAIN, TO THE P85 SUBUNIT OF
 CC -1- SUBUNIT: ASSOCIATES THROUGH ITS SH3 DOMAIN, TO THE P85 SUBUNIT OF
 CC PHOSPHATIDYLINOSITOL 3-KINASE. INTERACTS WITH THE FYN-BINDING
 CC PROTEIN (FYN).
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
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